

82001

From: Schnizer, Holly
 Sent: Tuesday, December 10, 2002 9:30 AM
 To: STIC-Biotech/ChemLib
 Subject: seq. search for appl. no. 09/444,281

RECEIVED
 DEC 10 2002

Please search the commercial and interference databases for:

SEQ ID NOs: 35 and 36 and,

a peptide with the following sequence (SEQ ID NO: 35)(SEQ ID NO:27)(SEQ ID NO:35)

Thank you.

Holly Schnizer
 AU 1653
 CM1-9E09
 305-3722
 mailbox: CM1-9B01

SEARCHED
 (STIC)

9 E 0 9

Searcher: Point of Contact
 Phone: P. Sheppard
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 Location: _____
 Date Picked Up: _____
 Date Completed: 12/13/02
 Searcher Prep/Review: _____
 Clerical: _____
 Online time: _____

TYPE OF SEARCH:
 NA Sequences: _____
 AA Sequences: _____
 Structures: _____
 Bibliographic: _____
 Litigation: _____
 Full text: _____
 Patent Family: _____
 Other: _____

VENDOR/COST (where applic.)
 STN: _____
 DIALOG: _____
 Questel/Orbit: _____
 DRLink: _____
 Lexis/Nexis: _____
 Sequence Sys.: _____
 WWW/Internet: _____
 Other (specify): _____

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GenCore version 5.1.3
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OM protein - protein search, using sw model
 Run on: December 11, 2002, 15:37:24 ; Search time 28 Seconds

272.277 Million cell updates/sec

Title: US-09-444-281-35-27-35
 Perfect score: 241

Sequence: 1 ILKKWPWWPKRRKHEAPEPEAEPIMILKKWPWWPKRRK 37

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTRMBL 21: *
 2: SP_archea: *
 3: SP_bacteria: *
 4: SP_fungi: *
 5: SP_invertebrate: *
 6: SP_mammal: *
 7: SP_mhc: *
 8: SP_orcanelle: *
 9: SP_phage: *
 10: SP_plant: *
 11: SP_rrodent: *
 12: SP_virus: *
 13: SP_vertebrate: *
 14: SP_unclassified: *
 15: SP_virus: *
 16: SP_bacteriapl: *
 17: SP_archeapl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

DESCRIPTION

17	60	24.9	242	17	Q8TVMB8	08tvmb8	methanopyru
18	60	24.9	381	16	Q8R7E1	09a7e1	caulobacter
19	60	24.9	381	16	Q9IC5Y	09ic5y	tt virus. o
20	59	24.7	114	16	Q98C52	09x8c2	streptomyce
21	59	24.7	292	12	Q66765	066765	encephalomy
22	59	24.5	95	10	Q8IQN0	091qn0	arabidopsis
23	59	24.5	485	16	P72844	P72844	synchocyst
24	59	24.5	739	12	Q9RAQ3	09aq3	tt virus. o
25	58.5	24.3	521	10	Q9AEF3	09aef3	oryza sativ
26	58.5	24.3	1567	2	Q9ADM1	Q9adm1	polyangium
27	58	24.1	107	16	Q9RAE4	09xae4	streptomyce
28	58	24.1	513	11	Q63299	063299	rattus norv
29	58	24.1	646	11	Q63779	063779	rattus norv
30	58	24.1	879	11	Q8V79	08v79	homo sapien
31	58	24.1	1300	11	P97692	P97692	rattus norv
32	57.5	23.9	117	15	Q9RRR9	09yrr9	human immun
33	57.5	23.9	341	13	Q9D644	090644	gallus gall
34	57.5	23.9	3	3	Q94516	094516	schizosacch
35	57.5	23.9	444	4	Q9R40	Q9rc40	homo sapien
36	57.5	23.9	772	4	Q9BXY6	Q9bxy6	homo sapien
37	57.5	23.9	252	15	Q9TU37	Q9tu37	human immun
38	57	23.7	426	12	Q9RAQ7	Q9raq7	tt virus. o
39	57	23.7	970	11	Q88821	088821	mus musculu
40	57	23.7	11	11	Q70458	070458	mus musculu
41	56.5	23.4	157	5	Q9T0E8	Q9t0e8	drosophila
42	56.5	23.4	162	5	Q9W1W7	Q9w1w7	drosophila
43	56.5	23.4	532	15	Q9CK19	Q9ck19	pasteurella
44	56	23.2	252	15	Q9ITX8	Q9itx8	human immun
45	56	23.2	252	15	Q9ITV2	Q9itv2	human immun

ALIGNMENTS

RESULT 1

ID: Q9Y7V5 PRELIMINARY; PRT; 1245 AA.
 Q9Y7V5; 01-NOV-1999 (TREMBLrel. 12, Created)
 DT: 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT: 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE: Conidiospore surface protein.
 GN: CML1.
 OS: Trichoderma harzianum.
 OX: Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Trichoderma.
 NCBI_TaxID:5544;

[1] Q9Y7V5 PRELIMINARY; PRT; 1245 AA.
 SEQUENCE FROM N.A.
 STRAIN=ATCC 32173;
 MEDLINE=99343881; Pubmed=10413618;
 RA: Pavaresky M., Benhannou N., Ponce Noyola P., Bauw G., Ziv T.,
 Van Montagu M., Herrera Estrella A., Horwitz B.A.;
 RT: "neurodevelopmental regulation of cml1, a gene encoding a multidomain
 Conidiospore surface protein of Trichoderma.";
 RT: Fungal Genet. Biol. 27:88-99 (1999).

RL: EMBL; AJ13351; CAB0454.1;
 DR: HSSP; P01180; INPO;
 DR: InterPro; IPR01673; S_m1dd_repeat;
 DR: ProDom; P0066869; S_m1dd_repeat; 2;
 DR: InterPro; IPR01673; S_m1dd_repeat;
 DR: PROSITE; PS01346; CLAUDIN; UNKNOWN; 1;
 SQ: SEQUENCE: 1245 AA; 13524 MW; 3249C749AFA0CDF8 CRC64;

Query Match 29.3%; Score 70.5%; DB 3; Length 1245;
 Best Local Similarity 29.0%; Pred. No. 2, 3;
 Matches 9; Conservative 2; Mismatches 9; Indels 11; Gaps 1;
 Qy 4 KAPWPKWWPKRRKHEAPEPEAEPIMILKKWPWWPK 34
 Db 1185 RWWQWSWPRGRG-----CWWQWSW 1204

RESULT 2

Q9H31 PRELIMINARY; PRT; 746 AA.

ID Q9H31; AC Q9H31; DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE ORF1.

OS TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_TaxID=68887;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=TUN02;

RA Okamoto H.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [2] SEQUENCE FROM N.A.

RP STRAIN=TUN02;

RX MEDLINE=20456301; PubMed=11003468;

RA Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M., Iizuka H., Miyakawa Y., Mayumi M.;

RT "The entire nucleotide sequences of two distinct TT virus (TTV) isolates (TJN01 and TJN02) remotely related to the original TTV isolates.";

RT Arch. Virol. 145:1543-1559 (2000).

RL Arch. Virol. 145:1543-1559 (2000).

DR EMBL; AB028669; BA094878.1; -.

DR InterPro; IPR004219; TTVirus_Unknown.

DR Pfam; PF02956; TT_ORF1; 1.

SEQUENCE 746 AA; 88561 MW; E0B22953AE764E3E CRC64;

Query Match 28.0%; Score 67.5; DB 12; Length 746; Best Local Similarity 33.3%; Pred. No. 3.2; Matches 11; Conservative 2; Mismatches 5; Indels 15; Gaps 1;

QY 5 WPWWWWRKKEAEPEAEPIMILKKWPWWPRRK 37

|-Db 3 WGWWWWRR-----RWPARRWRRR 20

RESULT 3

Q9DUC4 PRELIMINARY; PRT; 723 AA.

ID Q9DUC4; AC Q9DUC4; DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE ORF1.

OS TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_TaxID=68887;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=MF_TTV9;

RA Okamoto H.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [2] SEQUENCE FROM N.A.

RP STRAIN=MF_TTV9;

RC MEDLINE=20534983; PubMed=11080484;

RA Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J., Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;

RT "Species-specific TT viruses in humans and nonhuman primates and their phylogenetic relatedness";

RT Virology 277: 368-379 (2000).

DR EMBL; AB041959; BAB19313.1; -.

DR InterPro; IPR001563; Serine_carbpept.

DR InterPro; IPR004219; TTVirus_Unknown.

DR Pfam; PF02856; TT_ORF1; 1.

SEQUENCE 723 AA; 85393 MW; 232D003098766344 CRC64;

Query Match 27.8%; Score 67; DB 12; Length 723;

RESULT 4

Q9IRD8 PRELIMINARY; PRT; 175 AA.

ID Q9IRD8; AC Q9IRD8; DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE ORF3.

OS TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_TaxID=68887;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=L03;

RA Liu Z.H., Luo K.X., Hu J., He H.T.;

RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF371370; AAK54733.1; -.

DR InterPro; IPR004219; TTVirus_Unknown.

DR Pfam; PF02956; TT_ORF1; 1.

SEQUENCE 175 AA; 22073 MW; 5212D7PA3FD72F81 CRC64;

Query Match 26.6%; Score 64; DB 12; Length 175; Best Local Similarity 33.3%; Pred. No. 2.1; Matches 11; Conservative 2; Mismatches 4; Indels 16; Gaps 2;

QY 5 WPWWWWRKKEAEPEAEPIMILKKWPWWPRRK 37

|-Db 3 WSWWWWRRR-----WWRRRRR 19

RESULT 5

Q9DT80 PRELIMINARY; PRT; 49 AA.

ID Q9DT80; AC Q9DT80; DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE ORF1 (Fragment).

OS TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.

OX NCBI_TaxID=68887;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=TTM9;

RC MEDLINE=20568739; PubMed=11118348;

RA Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J., Sai T., Sugai Y.;

RT "TT virus mRNAs detected in the bone marrow cells from an infected individual";

RT Biochem. Biophys. Res. Commun. 279:700-707 (2000).

DR EMBL; AB050449; BAB1930.1; -.

RT NON_TER 49 49

SQ SEQUENCE 49 AA; 7225 MW; 1DA6F81AB69AA43 CRC64;

Query Match 26.1%; Score 63; DB 12; Length 49; Best Local Similarity 30.3%; Pred. No. 0.79; Matches 10; Conservative 3; Mismatches 4; Indels 16; Gaps 2;

QY 5 WPWWWWRKKEAEPEAEPIMILKKWPWWPRRK 37

|-Db 3 WTWWWWRRR-----WPWRRR 19

RESULT 6

Q928B7

ID	Q92BB7	PRELIMINARY;	PRT;	192 AA.
AC	Q228B7;			
DT	01-MAY-1999 (TREMBrel. 10, Last sequence update)			
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)			
DE	CT277. SIMILARITY (CP0426 protein).			
GN	CP0426 OR CP0426 OR CP0327.			
OS	Chlamydia pneumoniae (Chlamydophila pneumoniae).			
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.			
OX	NCBI_TaxID=83558;			
RN	[1]	SEQUENCE FROM N. A.		
RP	STRAIN=CWL039;			
RX	MEDLINE=99206606; PubMed=10192388;			
RA	Kelman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,			
RA	Olinger L., Grimwood J., Davis R.W., Stephens R.S.,			
RT	*Comparative genomes of Chlamydia pneumoniae and <i>C. trachomatis</i> .";			
RL	Nat. Genet. 21:385-389(1999).			
RN	[2]	SEQUENCE FROM N. A.		
RP	STRAIN=FR39;			
RX	MEDLINE=20150255; PubMed=10684935;			
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,			
RA	White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,			
RA	Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,			
RA	Gwynn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,			
RA	Eisen J., Fraser C.M.,			
RT	"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia			
RT	pneumoniae AR39.";			
RL	Nucleic Acids Res. 28:1397-1406(2000).			
RN	[3]	SEQUENCE FROM N. A.		
RP	STRAIN=J138;			
RX	MEDLINE=20330349; PubMed=10871362;			
RA	Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,			
RA	"Comparison of whole genome sequences of Chlamydia pneumoniae J138			
RT	from Japan and CW029 from USA.";			
RL	Nucleic Acids Res. 28:2311-2314(2000).			
DR	EMBL; AAB00125; AAD1870.1; -;			
DR	EMBL; AAB00219; AAF38182.1; -;			
DR	EMBL; AAB002346; BAA9834.1; -;			
DR	TIGR; CP0327; -;			
KW	Complete proteome.			
SEQUENCE	192 AA;	21464 MW;	9C38C329AEDDB76F CRC64;	
Query Match	26.1%	Score 63;	DB 16;	Length 192;
Best Local Similarity	42.3%	Pred. No. 3;		
Matches	11;	Conservative	4;	Mismatches 11;
QY	5 WPPWPWPKRKHEAPEAEPIMILKKWPWWPKR 30			
Db	138 WPPWPKKRQTEKLPKGEGICFLSSAYP 163			
RESULT 7				
ID	Q9P81	PRELIMINARY;	PRT;	748 AA.
AC	Q9P81;			
DT	01-MAR-2001 (TREMBrel. 16, Created)			
DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)			
DE	ORF1.			
OS	TT virus.			
OC	Viruses; ssDNA viruses; unclassified ssDNA viruses.			
OX	NCBI_TaxID=58887;			
RN	[1]	SEQUENCE FROM N. A.		
RP	STRAIN=LYM9;			
RX	MEDLINE=20568739; PubMed=11118348;			
RA	Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J.,			
RA	Sai T., Sugai Y.,			
RT	"TT virus mRNAs detected in the bone marrow cells from an infected			
RESULT 8				
ID	Q91D04	PRELIMINARY;	PRT;	750 AA.
AC	Q91D04;			
DT	01-DEC-2001 (TREMBrel. 19, Created)			
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)			
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)			
DE	ORF1.			
OS	TT virus.			
OC	Viruses; ssDNA viruses; unclassified ssDNA viruses.			
OX	NCBI_TaxID=6887;			
RP	SEQUENCE FROM N. A.			
RX	MEDLINE=87064324; PubMed=3023845;			
RA	D'Ambrusio E., Waltzkin S.D., Whitney F.R., Saleem A., Furano A.V.,			
RT	"Structure of the highly repeated, long interspersed DNA family (LINE			
RT	or LINE) of the rat.";			
RT	Mol. Cell. Biol. 6:411-424(1986).			
DR	EMBL; M13100; AAB66045.1; -;			
DR	InterPro; IPR00556; Lipocalin_cytfabp.			
DR	PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.			
KW	Hypothetical protein.			

RT	characterization of North American ovine lentiviruses."
RL	Submitted (JUL-1996) to the EMBL/GenBank/DDJB databases.
DR	EMBL; U64439; AAB08725.1; -
DR	InterPro; IPR000328; Env_GP41.
DR	Pfam; PF00517; GP41; 1.
KW	transmembrane.
SQ	SEQUENCE 985 AA; 113794 MW; 3197258 EDBDE3597 CRC64;
Query Match	25.3%; Score 61; DB 15; Length 985;
Best Local Similarity	23.4%; Pred. No. 25;
Matches	18; Conservative 7; Mismatches 8; Indels 44; Gaps 5;
Qy	1 IIKK-----WFW-----WP-----WRRHEAEEAE----- 21
Db	163 IJKRYKQDMPWNTYHWPLWOMENMRQWMKENERKEYGRTNKTEDIDLLAGKIRGRFC 222
Qy	22 ---PIMLK--KWPWMP 33
Db	223 VPYPALLKQTWKWCMWP 239
RP	SEQUENCE FROM N.A.
RC	STRAIN=T-TTV6;
RX	MEDLINE=20534983; PubMed=11080484;
RA	Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
RA	Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.,
RT	"Specie-specific TT viruses in humans and nonhuman primates and their phylogenetic relatedness";
RT	Virology 277:368-378 (2000).
RL	EMBL; AB041957; BAB19308.1; -.
DR	InterPro; IPR04219; TTVirus_Unk.
DR	Pfam; PF02956; TT_ORF1; 1;
DR	PFAM; PF02956; TT_ORF1; 1; 86132 MW; 9ED818D6BECFA5D3 CRC64;
RP	SEQUENCE FROM N.A.
RC	STRAIN=T-TTV6;
RX	MEDLINE=20534983; PubMed=11080484;
RA	Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
RA	Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.,
RT	"Specie-specific TT viruses in humans and nonhuman primates and their phylogenetic relatedness";
RT	Virology 277:368-378 (2000).
Qy	5 WPW---WPMRKHEAEEAPIMILKKWPW---PWRK 37
Db	3 WPMRKHEAEEAPIMILKKWPW---PRWRRWRRRTWRR 31
RESULT 15	
Q98414	
ID	098414 PRELIMINARY; PRT; 985 AA.
AC	Q98414;
DT	01-FEB-1997 (TREMBLrel. 02; Created)
DT	01-FEB-1997 (TREMBLrel. 02; Last sequence update)
DE	01-DEC-2001 (TREMBLrel. 19; Last annotation update)
DE	Envelope glycoprotein.
GN	ENV.
OS	Ovine lentivirus.
OC	Viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11663;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=85/34;
RX	MEDLINE=95135990; PubMed=7834396;
RA	Woodward T.M., Carlson J.O., de la Concha-Bermejillo A.,
RA	Demartini J.C.,
RT	"Biological and genetic changes in ovine lentivirus strains following passage in isogenic twin lambs.;"
RT	J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 8:124-133(1995).
RL	[2]
RN	SEQUENCE FROM N.A.
RC	STRAIN=85/34;
RC	Carlson J.O., Demartini J.C., Mwaengo D.M.,
RT	"Envelope glycoprotein nucleotide sequence and genetic

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:34:48 ; Search time 11 Seconds

Perfect score: 241 ; Sequence: 1 ILLKWPWWPWRKHEAEPEAEPIMILKKWPWWPWRK 37

Title: US-09-444-281-35-27-35
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	7.8	32.4	1 IND_C_BOVIN	P33046 bos taurus
2	25.7	144	1 YM3_BACST	P04553 bacillus st
3	24.7	2290	1 P01G_EMCV	P03304 encephalomy
4	23.7	711	1 MMIA_STRCO	P053902 streptomyce
5	23.0	55	1 ATPB_ANPBL	P50555 anas platyr
6	23.0	942	1 ENV_CAEVG	P31627 caprine art
7	23.0	990	1 ENV_OMVVS	P16899 ovine lenti
8	22.8	715	1 YDQ5_MYCCTU	Q11025 mycobacteri
9	22.4	144	1 AP22_APITME	P35581 apis mellif
10	22.4	469	1 SYC1_MYCNU	P96862 mycobacteri
11	22.4	473	1 SYC1_MYCNU	P57909 mycobacteri
12	22.4	1173	1 VGL2_CVH22	P15423 human coron
13	22.2	1042	1 CORI_HUMAN	Q9Y9Q5 homo sapien
14	22.2	1113	1 CORI_MOUSE	Q9Z319 mus musculus
15	22.0	424	1 FDGC_SOVBN	P48628 glycine max
16	21.8	55	1 ATPB_AYVAM	Q9XK25 aythya amer
17	21.8	257	1 E434_ADP40	Q64865 human adeo
18	21.8	691	1 ITHG_ECOLI	P37643 escherichia
19	21.8	982	1 ENV_VILV	P03379 visna lenti
20	21.8	983	1 ENV_VILV	P35954 visna lenti
21	21.8	991	1 ENV_VILV2	P23423 visna lenti
22	21.8	1154	1 VGL2_IBV02	P12722 avian infec
23	21.8	1162	1 VGL2_IBV02	P11233 avian infec
24	21.8	1162	1 VGL2_IBV02	P12650 avian infec
25	21.8	1162	1 VGL2_IBV02	P12651 avian infec
26	21.8	1163	1 VGL2_IBV02	P05135 avian infec
27	21.6	68	1 Y121_BPT4	P02405 bacteriophaga
28	21.4	162	1 DSBB_NEIMA	Q9Jtag neisseria m
29	21.4	162	1 DSBB_NEIMA	Q9Jyc6 neisseria m
30	21.4	175	1 NUGG_ANASP	Q44241 anabena sp
31	21.4	443	1 FDGC_BRANA	P48627 brassica na
32	21.4	448	1 FDGC_BRATH	P46312 arabisopsis
33	21.4	989	1 ENV_VILV1	P23422 visna lenti

ALIGNMENTS

RESULT 1	ID	INDC_BOVIN	STANDARD;	PRT;	144 AA.
	ID	INDC_BOVIN			
	AC	P33046;			
	DT	01-OCT-1993 (Rel. 27, Created)			
	DT	01-OCT-1993 (Rel. 27, Last sequence update)			
	DT	01-NOV-1997 (Rel. 35, Last annotation update)			
	DE	Indolicidin precursor.			
	OS	Bos taurus (Bovine).			
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.			
	OC				
	OX	NCBI_TaxID:9913;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RC	SEQUENCE-Bone marrow;			
	RC	MEDLINE=92392368; PubMed=1520337;			
	RA	del Sal G., Storici P., Schneider C., Romeo D., Zanetti M.; RT			
	RA	"CDNA cloning of the neutrophil bactericidal peptide indolicidin."			
	RA	RT			
	RL	Biochem. Biophys. Res. Commun. 187:467-472(1992).			
	RN	[2]			
	RP	SEQUENCE OF 131-143.			
	RC	SEQUENCE-Neutrophilis;			
	RC	MEDLINE=92165771; PubMed=1537821;			
	RA	Collier M.E., Novotny M.J., Morris W.L., Tang Y.-Q., Smith W., RA			
	RA	"Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils";			
	RA	J. Biol. Chem. 267:4292-4295(1992).			
	CC	-1- FUNCTION: POTENT MICROMICIDAL ACTIVITY, ACTIVE AGAINST STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.			
	CC	-1- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.			
	CC	-1- PTM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.			
	CC	-1- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.			
	CC				
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	CC				
	CC	EMBL; X67340; CAA47755.1; -.			
	DR	PTR; JC1222; JC1222.			
	DR	P12722; IPR01894; Cathelicidin.			
	DR	InterPro; IPR00665; Cathelicidins; 1.			
	DR	ProDom; PD001838; Cathelicidin; 1.			
	DR	PROSITE; PS00946; CATHELICIDINS_1; 1.			
	DR	PROSITE; PS00947; CATHELICIDINS_2; 1.			
	KW	Antibiotic; Amidation; Signal.			
	FT	SIGNAL	1	29	POTENTIAL.
	FT	PROPEP	30	130	
	FT	PEPTIDE	131	143	INDOLICIDIN.
	FT	MOD_RES	30	30	PYRROLIDONE CARBOXYLIC ACID (BY

09um54 homo sapien
Q64331 mus musculus
Q11013 mycobacteri
Q09677 schizosaccha
Q8xdz7 escherichia
P1109 e menaquinina
R17593 encephalomy
P17594 encephalomy
Q02695 salmonella
Q9Jcx2 thermus the

RT "Structure and genetic variability of envelope glycoproteins of two
RT antigenic variants of caprine arthritis-encephalitis lentivirus.";
RL J. Virol. 65:5744-5750(1991).
RN [2]
RP

RA Knowles D.P.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

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CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>

DR PIR: M41307; VCLJC6;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.

KW Glycoprotein; Coat protein; Polyprotein; Transmembrane.

FT PEPTIDE 1 80 LEADER PEPTIDE.

FT CHAIN 81 630 SURFACE PROTEIN (POTENTIAL).

FT DOMAIN 631 659 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 650 799 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 800 820 POTENTIAL.

FT CARBOHYD 821 942 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 503 503 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 942 AA; 108437 MW; 550E1F3D355F4A CRC64;

Query Match 23 0%; Score 55.5; DB 1; Length 942;

Best Local Similarity 21.4%; Pred. No. 18; Length 942;

Matches 15; Conservative 7; Mismatches 9; Indels 39; Gaps 4;

QY 3 KKWYW--WP-----WRRKHEAEAE-----PIMI 25

Db 143 ENWPWNTYHWPLWOMENVRYWLKENAIAENKKRNSTKKGIEELLAGTIRGRFCVYPYPFAL 202

QY 26 LK--KWPWMP 33

Db 203 LKCTRKWCWYP 212

RESULT 7

ENV_OMVVS ID ENV_OMVVS STANDARD; PRT; 990 AA.

AC P1899; 01-AUG-1990 (Rel. 15, created)
DT 01-AUG-1990 (Rel. 15, last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE ENV Polyprotein precursor (Coat polyprotein).

DR ENV

RA N

OS Ovine lentivirus (strain SA-OMV).

OC Viruses; Retroviridae; Lentivirus.

OX NCBI TaxID=1164; RN

RP [1] SEQUENCE FROM N.A.

DR MEDLINE=90223989; PubMed=2158181;

RA Querat G., Audoly G., Sonigo P.; Vigne R.;

RT "Nucleotide sequence analysis of SA-OMV: phylogenetic history of lentiviruses.";

RT Virology 175:434-447(1990).

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CC or send an email to license@isb-sib.ch).

DR EMBL: M34193; AAA46783.1; -.

DR PIR: M34193; G46335; G46335.

DR HIV; M34193; ENVSOMVVSACG.

DR InterPro: IPR000328; Env_GP41.

DR Pfam: PF00517; GP41; 1.

FT PEPTIDE 1 101 LEADER PEPTIDE.

FT CHAIN 102 662 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT DOMAIN 663 990 TRANSMEMBRANE GLYCOPROTEIN.

FT TRANSMEM 842 863 POTENTIAL.

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 207 259 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 490 490 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 526 526 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 550 550 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 567 567 N-LINKED (GLCNAC. . .) (POTENTIAL).

QY 3 KKPW-----WRRKHEAEAE-----PIMI 25

Best Local Similarity 20.0%; Pred. No. 19; Length 990;

Matches 14; Conservative 9; Mismatches 8; Indels 39; Gaps 4;

Db 174 QEWPMNTYHWPLWOMENRQWMKENEKEYTSRNNKTKEDIDALLAGKIRGRFCVYPYPFAL 233

QY 26 LK--KWPWMP 33

Db 234 LKCEEWCWYP 243

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Copyright (c) 1993 - 2002 Compugen Ltd. Gencore version 5.1.3

M protein - protein search, using sw model

run on: December 11, 2002, 15:38:09 : Search time 19 seconds
 (without alignments)
 187,209 Million cell updates/sec

title: US-09-444-281-35-27-35
 perfect score: 241
 sequence: IILKKWPWPWPWRKHEAEPEAERIMILKKWPWPWPWRK 37

scoring table: BIOSIM62
 searched: Gapct 10.0 , Gapext 0.5
 283224 seqs, 91134422 residues

total number of hits satisfying chosen parameters: 283224

minimum DB seq length: 0
 maximum DB seq length: 200000000

post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

result No.	Score	Query Match	Length	DB ID	Description
1	78	32.4	144	1 JC1222	indolicidin precursor
2	63	26.1	192	2 H06543	hypothetical protein
3	63	26.1	192	2 D12081	conserved hypothetical protein
4	62	25.7	314	2 SA3916	hypothetical protein
5	60	24.9	381	2 B87470	hypothetical protein
6	59.5	24.7	114	2 T6208	hypothetical protein
7	59.5	24.7	2290	1 GNYIE	hypothetical polypeptide
8	59	24.5	95	2 E84447	protein F5B14.5 [1]
9	59	24.5	485	2 SA74708	hypothetical protein
10	58	24.1	107	2 T35634	hypothetical protein
11	58	24.1	513	2 S21976	probable RNA-directed protein
12	57.5	23.9	376	2 T40591	hypothetical protein
13	57	23.7	711	2 C0046	antibiotic transposon protein
14	56	23.2	452	2 T28094	hypothetical protein
15	55.5	23.0	527	2 S33068	myosin heavy chain
16	55.5	23.0	990	1 G44335	env polyprotein
17	55.5	23.0	1840	2 A52827	myosin heavy chain
18	55	22.8	245	2 C09459	transcription regulator
19	55	22.8	352	2 S74458	hypothetical protein
20	55	22.8	715	2 B77041	probable myosin protein
21	54.5	22.6	134	2 E77532	hypothetical protein
22	54.5	22.6	340	2 PH0217	reverse transcriptase
23	54.5	22.6	451	2 S34401	hypothetical protein
24	54.5	22.6	547	2 T45635	hypothetical protein
25	54	22.4	144	2 S5331	apidaecin 22 precursor
26	54	22.4	187	2 AB1647	hypothetical protein
27	54	22.4	469	2 B70607	probable cysteine protein
28	54	22.4	473	2 S4949	probable cysteinyl E2 glycoprotein
29	54	22.4	1173	1 VGHHC	probable cysteinyl E2 glycoprotein

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Gencore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
M protein - protein search, using sw model
run on: December 11, 2002, 15:38:09 : Search time 19 seconds
(without alignments)
187.209 Million cell updates/sec
title: US-09-444-281-35-27-35
perfect score: 241
sequence: 1 IILKKWPWPWPWRKHEAEPEAERIMILKKWPWPWRK 37
scoring table: BIOS62
Gapop 10.0 , Gapext 0.5
searched: 283224 seqs, 91134422 residues

LIGNMENTS	15	hypothetical prote
	99	low-density lipoprote
	43	hypothetical prote
	42	hypothetical F420-redu
	52	coenzyme Q420-redu
	52	omega-6 desaturase
	52	Shb-like adapter p
	52	hypothetical prote
	61	glycine Cleavage s
	26	capsid polyprotein
	26	H ⁺ -transporting tw
	18	chloramphenicol o
	16	hypothetical prote
	65	transcription fact
	89	hypothetical prote
	64	hypothetical prote
		peplomeric polypro

A;C-Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999	OY	5 WP-----WWPWRKHEAPEAPIMIK---KWPWKPW 34	
A;Accession: A03906; JN0383		: : :	
R;Palmenberg, A.C.; Kirby, E.M.; Janda, M.R.; Drake, N.L.; Duke, G.M.; Potratz, K.F.; Co		: : :	
Nucleic Acids Res. 12, 2965-2985, 1984	-----	-----PVLVITDVGGESWWWW 81	
A;Title: The nucleotide and deduced amino acid sequences of the encephalomyocarditis virus			
A;Reference number: A03906; MUID:84169586; PMID:6324136			
A;Molecule type: genomic RNA	RESULT 9	S74708	
A;Residues: 1-2280 <PAl>		hypothetical protein slr1306 - <i>Synechocystis</i> sp. (strain PCC 6803)	
A;Cross-references: GB:X00463; NID:961034; PIDN:CA25152 1; PID:961035		C;Species: <i>Synechocystis</i> sp.	
R;Petrov, N.A.; Chizhikov, V.E.; Blinov, V.M.; Karginov, V.A.; Mikryukov, N.N.; Gutorov,		A;Variety: PCC 6803	
Bloorg, Khim. 10, 274-279, 1984		C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999	
A;Title: Nucleotide sequence of the 3'-terminus of encephalomyocarditis virus RNA.		C;Accession: S74708	
A;Reference number: JN0383; MUID:85022788; PMID:6091680		R;Fukeno, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,	
A;Accession: JN0383		O., K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas	
A;Molecule type: genomic RNA		u, S.; Okumura, S.; Yamada, M.; Yas	
A;Residues: 1337-1396, L', 1398-1517, 'A', 1519-1536, 'E', 1538-1556, 'S', 1558-1611, 'T', 1613-1		A;Title: Sequence analysis of the genome of the unicellular cyanobacterium <i>Synechocys</i>	
A;Note: the authors translated the codon CAU for residue 713 as Thr and AAC for residue		s. A;Reference number: S74322; MUID:97061201; PMID:8905331	
C;Superfamily: foot-and-mouth disease virus genome polyprotein		A;Accession: S74708	
C;Keywords: coat protein; core protein; genome-linked protein; hydrolase; nucleotidyltra		A;Status: preliminary	
F;1-67/Domain: leader peptide #status predicted <LDP>		A;Molecule type: DNA	
F;68-136/Product: coat protein VP4 #status predicted <VP4>		A;Residues: 1-485 <KAN>	
F;137-391/Product: coat protein VP2 #status predicted <VP2>		A;Cross-references: EMBL:D90901; GB:AB001339; NID:91651897; PIDN:BA016859; 1; PID:di01	
F;392-622/Product: coat protein VP3 #status predicted <VP3>		A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996	
F;623-710/Product: coat protein VP1 #status predicted <VP1>		A;Accession: S74708	
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F;1606-1625/Product: proteinase I #status predicted <PNS>		A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996	
F;1626-1830/Product: proteinase II #status predicted <PVP>		A;Accession: S74708	
F;1831-2290/Product: RNA-directed RNA polymerase #status predicted <RDP>		A;Status: preliminary	
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Matches 11; Conservative 6; MisMatches 8; Indels 17; Gaps 1;		Best Local Similarity 29.3%; Pred. No. 8.6; Mismatches 12; Conservative 6; MisMatches 5; Indels 18; Gaps 2;	
QY 6 PWMPWPKHKEAPEAEPIT-----MLKKWP 30	QY 6 PW-----WPKHKEAPEAEPIM---ILKK 28	QY 6 PW-----WPKHKEAPEAEPIM---ILKK 28	
Db 967 PWNPWKNTYQAVLRAEPCKRTMDIYKVRPFLPKVKEWP 1008	Db 41 PWDQDWGLWALSGLGIVIWRWRRHHAPPEQOKMLTPEVLOQ 81	Db 41 PWDQDWGLWALSGLGIVIWRWRRHHAPPEQOKMLTPEVLOQ 81	
RESULT 9	Query Match	24.1%; Score 58; DB 2; Length 107;	
Best Local Similarity 50.0%; Pred. No. 2.3; Mismatches 10; Conservative 2; MisMatches 8; Indels 0; Gaps 0;		Query Match	24.1%; Score 58; DB 2; Length 107;
Matches 10; Conservative 2; MisMatches 8; Indels 0; Gaps 0;		Best Local Similarity 50.0%; Pred. No. 2.3; Mismatches 10; Conservative 2; MisMatches 8; Indels 0; Gaps 0;	
QY 3 KKKWPKWPKHKEAPEAEP 22	QY 3 KKKWPKWPKHKEAPEAEP 22	QY 3 KKKWPKWPKHKEAPEAEP 22	
Db 79 RKWPKWPKPERPSAEEPDATP 98	Db 79 RKWPKWPKPERPSAEEPDATP 98	Db 79 RKWPKWPKPERPSAEEPDATP 98	
RESULT 10	Query Match	24.1%; Score 58; DB 2; Length 107;	
Best Local Similarity 50.0%; Pred. No. 2.3; Mismatches 10; Conservative 2; MisMatches 8; Indels 0; Gaps 0;		Query Match	24.1%; Score 58; DB 2; Length 107;
Matches 10; Conservative 2; MisMatches 8; Indels 0; Gaps 0;		Best Local Similarity 50.0%; Pred. No. 2.3; Mismatches 10; Conservative 2; MisMatches 8; Indels 0; Gaps 0;	
QY 3 KKKWPKWPKHKEAPEAEP 22	QY 3 KKKWPKWPKHKEAPEAEP 22	QY 3 KKKWPKWPKHKEAPEAEP 22	
Db 79 RKWPKWPKPERPSAEEPDATP 98	Db 79 RKWPKWPKPERPSAEEPDATP 98	Db 79 RKWPKWPKPERPSAEEPDATP 98	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
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A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
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C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
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A;Map position: 1		A;Map position: 1	
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A;Status: preliminary		A;Status: preliminary	
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A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
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RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:	
A;Map position: 1		A;Map position: 1	
RESULT 11	Query Match	24.5%; Score 59; DB 2; Length 95;	
Best Local Similarity 21.3%; Pred. No. 1.6; Mismatches 5; Conservative 4; Indels 28; Gaps 3; MisMatches 10;		Query Match	24.5%; Score 59; DB 2; Length 95;
A;Gene: F5D14.5		A;Gene: F5D14.5	
A;Status: preliminary		A;Status: preliminary	
A;Molecule type: DNA		A;Molecule type: DNA	
A;Residues: 1-95 <STO>		A;Residues: 1-95 <STO>	
A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141		A;Cross-references: GB:AE005172; NID:98920603; PIDN:AAF81325.1; GSPDB:GN00141	
C;Genetics:		C;Genetics:</	

us-09-444-281-35-27-35.rpr

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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 11, 2002, 15:39:44 ; Search time 11 Seconds

(without alignments) updates/sec 54.633 Million cell updates/sec

Title: US-09-444-281-35-27-35

Perfect score: 241

Sequence: 1 ILKKWPWWPWRKHEAEPERPIMLKKWPWWPWRK 37

Scoring table: BLOSUM62

Gapop 10.0 , gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 45 summaries

Database : Published Applications_AA_*

1: /cgn2_6/ptodata/2/pupcaa/US08_NEW_PUB.pep;*

2: /cgn2_6/ptodata/2/pupcaa/PCT_NEW_PUB.pep;*

3: /cgn2_6/ptodata/2/pupcaa/US06_NEW_PUB.pep;*

4: /cgn2_6/ptodata/2/pupcaa/US07_NEW_PUB.pep;*

5: /cgn2_6/ptodata/2/pupcaa/US07_PUBCOMB.pep;*

6: /cgn2_6/ptodata/2/pupcaa/US07_PUBCOMB.pep;*

7: /cgn2_6/ptodata/2/pupcaa/PCTUS_PUBCOMB.pep;*

8: /cgn2_6/ptodata/2/pupcaa/US08_PUBCOMB.pep;*

9: /cgn2_6/ptodata/2/pupcaa/US09_NEW_PUB.pep;*

10: /cgn2_6/ptodata/2/pupcaa/US09_PUBCOMB.pep;*

11: /cgn2_6/ptodata/2/pupcaa/US10_NEW_PUB.pep;*

12: /cgn2_6/ptodata/2/pupcaa/US10_PUBCOMB.pep;*

13: /cgn2_6/ptodata/2/pupcaa/US60_NEW_PUB.pep;*

14: /cgn2_6/ptodata/2/pupcaa/US60_PUBCOMB.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

US-09-030-619-104

; Sequence 104, Application US/09030619B

; Patent No. US2002005061A1

; GENERAL INFORMATION:

; APPLICANT: Krieger, Timothy J.

; APPLICANT: Taylor, Robert

; APPLICANT: Erfile, Douglas

; APPLICANT: Fraser, Janet R.

; APPLICANT: West, Michael H.P.

; APPLICANT: Menicoli, Patricia J.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

; FILE REFERENCE: 660081406

; CURRENT APPLICATION NUMBER: US/09/030,619B

; NUMBER OF SEQ ID NOS: 232

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 104

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Cationic Peptide Analogue

; US-09-030-619-104

Query Match Best Local Similarity 58.7%; Score 141.5; DB 10; Length 28; Matches 20; Conservative 2; Mismatches 1; Indels 11; Gaps 1;

QY 4 KWPWWPWRKHEAEPERPIMLKKWPWWPWRK 37

Db 3 RWPWWPWRK-----ILMRWPWWPWRK 25

Sequence 104, App

Sequence 50, App

Sequence 69, App

Sequence 52, App

Sequence 51, App

Sequence 95, App

Sequence 99, App

Sequence 72, App

Sequence 108, App

Sequence 47, App

Sequence 67, App

Sequence 112, App

Sequence 53, App

Sequence 107, App

Sequence 109, App

Sequence 54, App

Sequence 110, App

Sequence 73, App

Sequence 41, App

RESULT 2

US-09-030-619-50

; Sequence 50, Application US/09030619B

; Patent No. US2002005061A1

; GENERAL INFORMATION:

; APPLICANT: Krieger, Timothy J.

RESULT 8
 US-09-030-619-72
 Sequence 72, Application US/09030619B
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Kriger, Timothy J.
 ;
 ; APPLICANT: Taylor, Robert
 ;
 ; APPLICANT: Erfile, Douglas
 ;
 ; APPLICANT: Fraser, Janet R.
 ;
 ; APPLICANT: McNicol, Patricia J.
 ;
 ; APPLICANT: West, Michael H.P.
 ;
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 ; INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
 ; WITH ANTIBIOTICS
 ;
 ; FILE REFERENCE: 660081.406
 ; CURRENT APPLICATION NUMBER: US/09/030.619B
 ; CURRENT FILING DATE: 1998-02-25
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ;
 ; SEQ ID NO 95
 ; LENGTH: 13
 ;
 ; TYPE: PRT
 ;
 ; ORGANISM: Artificial sequence
 ;
 ; FEATURE:
 ;
 ; OTHER INFORMATION: Cationic Peptide Analogue
 ;
 ; US-09-030-619-95
 ;
 ; Query Match 37.8%; Score 91; DB 10; Length 13;
 ; Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 ; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 Qy 1 ILKWKWPWPKRK 13
 Db 1 ILKWKWPWPKRK 13

RESULT 7
 US-09-030-619-99
 Sequence 99, Application US/09030619B
 ;
 ; PATENT NO. US20020035061A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Kriger, Timothy J.
 ;
 ; APPLICANT: Taylor, Robert
 ;
 ; APPLICANT: Erfile, Douglas
 ;
 ; APPLICANT: Fraser, Janet R.
 ;
 ; APPLICANT: McNicol, Patricia J.
 ;
 ; APPLICANT: West, Michael H.P.
 ;
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 ; INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
 ; WITH ANTIBIOTICS
 ;
 ; FILE REFERENCE: 660081.406
 ; CURRENT APPLICATION NUMBER: US/09/030.619B
 ; CURRENT FILING DATE: 1998-02-25
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ;
 ; SEQ ID NO 99
 ; LENGTH: 13
 ;
 ; TYPE: PRT
 ;
 ; ORGANISM: Artificial sequence
 ;
 ; FEATURE:
 ;
 ; OTHER INFORMATION: Cationic Peptide Analogue
 ;
 ; US-09-030-619-99
 ;
 ; Query Match 37.8%; Score 91; DB 10; Length 13;
 ; Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 ; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 Qy 1 ILKWKWPWPKRK 13
 Db 1 ILKWKWPWPKRK 13

RESULT 8
 US-09-030-619-108
 Sequence 108, Application US/09030619B
 ;
 ; PATENT NO. US20020035061A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Kriger, Timothy J.
 ;
 ; APPLICANT: Taylor, Robert
 ;
 ; APPLICANT: Erfile, Douglas
 ;
 ; APPLICANT: Fraser, Janet R.
 ;
 ; APPLICANT: McNicol, Patricia J.
 ;
 ; APPLICANT: West, Michael H.P.
 ;
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 ; INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
 ; WITH ANTIBIOTICS
 ;
 ; FILE REFERENCE: 660081.406
 ; CURRENT APPLICATION NUMBER: US/09/030.619B
 ; CURRENT FILING DATE: 1998-02-25
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ;
 ; SEQ ID NO 108
 ; LENGTH: 14
 ;
 ; TYPE: PRT
 ;
 ; ORGANISM: Artificial sequence
 ;
 ; FEATURE:
 ;
 ; OTHER INFORMATION: Cationic Peptide Analogue
 ;
 ; US-09-030-619-108
 ;
 ; Query Match 37.8%; Score 91; DB 10; Length 14;
 ; Best Local Similarity 100.0%; Pred. No. 2e-05;
 ; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 Qy 1 ILKWKWPWPKRK 13
 Db 1 ILKWKWPWPKRK 13

RESULT 9
 US-09-030-619-108
 Sequence 108, Application US/09030619B
 ;
 ; PATENT NO. US20020035061A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Kriger, Timothy J.
 ;
 ; APPLICANT: Taylor, Robert
 ;
 ; APPLICANT: Erfile, Douglas
 ;
 ; APPLICANT: Fraser, Janet R.
 ;
 ; APPLICANT: McNicol, Patricia J.
 ;
 ; APPLICANT: West, Michael H.P.
 ;
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 ; INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
 ; WITH ANTIBIOTICS
 ;
 ; FILE REFERENCE: 660081.406
 ; CURRENT APPLICATION NUMBER: US/09/030.619B
 ; CURRENT FILING DATE: 1998-02-25
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ;
 ; SEQ ID NO 108
 ; LENGTH: 14
 ;
 ; TYPE: PRT
 ;
 ; ORGANISM: Artificial sequence
 ;
 ; FEATURE:
 ;
 ; OTHER INFORMATION: Cationic Peptide Analogue
 ;
 ; US-09-030-619-108
 ;
 ; Query Match 37.8%; Score 91; DB 10; Length 14;
 ; Best Local Similarity 100.0%; Pred. No. 2e-05;
 ; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 Qy 1 ILKWKWPWPKRK 13
 Db 1 ILKWKWPWPKRK 13

RESULT 10
 US-09-030-619-47
 Sequence 47, Application US/09030619B
 ;
 ; PATENT NO. US20020035061A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Kriger, Timothy J.
 ;
 ; APPLICANT: Taylor, Robert
 ;
 ; APPLICANT: Erfile, Douglas
 ;
 ; APPLICANT: Fraser, Janet R.
 ;
 ; APPLICANT: West, Michael H.P.
 ;
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 ; INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
 ; WITH ANTIBIOTICS
 ;
 ; FILE REFERENCE: 660081.405
 ; CURRENT APPLICATION NUMBER: US/09/030.619B
 ; CURRENT FILING DATE: 1998-02-25
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ;
 ; SEQ ID NO 72
 ; LENGTH: 14
 ;
 ; TYPE: PRT
 ;
 ; ORGANISM: Artificial sequence
 ;
 ; FEATURE:
 ;
 ; OTHER INFORMATION: Indolicidin Analogue
 ;
 ; US-09-030-619-72
 ;
 ; Query Match 37.8%; Score 91; DB 10; Length 14;
 ; Best Local Similarity 100.0%; Pred. No. 2e-05;
 ; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 Qy 1 ILKWKWPWPKRK 13
 Db 1 ILKWKWPWPKRK 13

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 47

LENGTH: 21

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Indolicidin Analogue

US-09-030-619-47

RESULT 11

Query Match	Score	DB	Length	Best Local Similarity	Pred.	Mismatches	Indels	Gaps
Sequence 67, Application US/09030619B	36.3%	10	21	60.0%	8.1e-05	1	0	1
Patent No. US20020035061A1								

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Erfile, Douglas

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 67

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Indolicidin Analogue

US-09-030-619-67

RESULT 12

Query Match	Score	DB	Length	Best Local Similarity	Pred.	Mismatches	Indels	Gaps
Sequence 112, Application US/09030619B	36.1%	10	12	100.0%	5.1e-05	0	0	0
Patent No. US20020035061A1								

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Erfile, Douglas

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 47

LENGTH: 21

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Indolicidin Analogue

US-09-030-619-47

RESULT 13

Query Match	Score	DB	Length	Best Local Similarity	Pred.	Mismatches	Indels	Gaps
Sequence 53, Application US/09030619B	35.7%	10	12	100.0%	6.7e-05	0	0	0
Patent No. US20020035061A1								

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Erfile, Douglas

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 53

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Indolicidin Analogue

US-09-030-619-53

RESULT 14

Query Match	Score	DB	Length	Best Local Similarity	Pred.	Mismatches	Indels	Gaps
Sequence 107, Application US/09030619B	35.7%	10	13	100.0%	7.3e-05	0	0	0
Patent No. US20020035061A1								

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Erfile, Douglas

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 53

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Indolicidin Analogue

US-09-030-619-53

TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

TITLE OF INVENTION: WITH ANTIBIOTICS

FILE REFERENCE: 660081_406

CURRENT APPLICATION NUMBER: US/09/030,619B

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 107

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Cationic Peptide Analogue

US-09-030-619-107

RESULT 15
 US-09-030-619-109
 Sequence 109, Application US/09030619B
 Patent No. US20020035061A1
 GENERAL INFORMATION:
 APPLICANT: Krieger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erflie, Douglas
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.
 APPLICANT: McNicol, Patricia J.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
 TITLE OF INVENTION: WITH ANTIBIOTICS
 FILE REFERENCE: 660081_406
 CURRENT APPLICATION NUMBER: US/09/030,619B
 CURRENT FILING DATE: 1998-02-25
 NUMBER OF SEQ ID NOS: 232
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 109
 LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Cationic Peptide Analogue

US-09-030-619-109

Query Match 35.7%; Score 86; DB 10; Length 13;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 QY 7 WWPWRRKHEAPEAPEPIMILKKWPWNPWRRK 37
 Db 1 WW-----KKWPWNPWRRK 13

Search completed: December 11, 2002, 15:43:29
 Job time : 11 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 11, 2002, 15:37:49 ; Search time 15 Seconds
 (without alignments)
 72.577 Million cell updates/sec

Title: US-09-444-281-35-27-35
 Perfect score: 241
 Sequence: 1 IILKKWPKWPKRKKHAEPEAEPERIMILKKWPKWPKR 37
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*

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6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	133.5	55.4	63	4 US-09-099-631A-12	Sequence 12, Appl
2	99.5	41.3	16	4 US-08-002-054B-38	Sequence 38, Appl
3	99	41.1	21	4 US-08-015-314-54	Sequence 54, Appl
4	98	40.7	21	4 US-08-015-314-56	Sequence 56, Appl
5	93.8	38.8	20	4 US-08-015-314-55	Sequence 55, Appl
6	91	37.8	13	4 US-08-015-314-30	Sequence 30, Appl
7	91	37.8	13	4 US-08-015-314-62	Sequence 62, Appl
8	91	37.8	13	4 US-08-015-314-63	Sequence 63, Appl
9	91	37.8	13	4 US-08-015-314-64	Sequence 64, Appl
10	91	37.8	13	4 US-09-042-071-36	Sequence 36, Appl
11	91	37.8	14	5 US-08-015-314-57	Sequence 57, Appl
12	89	36.9	15	4 US-08-002-054B-40	Sequence 40, Appl
13	87.5	36.3	21	4 US-08-015-314-46	Sequence 46, Appl
14	87	36.1	12	4 US-08-015-314-55	Sequence 52, Appl
15	86	35.7	12	4 US-08-015-314-74	Sequence 74, Appl
16	86	35.7	12	4 US-08-002-054B-5	Sequence 5, Appl
17	86	35.7	13	4 US-08-015-314-51	Sequence 51, Appl
18	86	35.7	13	4 US-08-015-314-58	Sequence 58, Appl
19	86	35.7	13	4 US-08-002-054B-34	Sequence 34, Appl
20	86	35.7	14	5 US-08-015-314-59	Sequence 59, Appl
21	85.5	35.5	16	4 US-08-002-054B-11	Sequence 11, Appl
22	85	35.3	12	4 US-08-015-314-69	Sequence 69, Appl
23	85	35.3	13	4 US-08-015-314-38	Sequence 38, Appl
24	85	35.3	13	4 US-08-015-314-45	Sequence 45, Appl
25	85	35.3	13	4 US-08-002-054B-1	Sequence 1, Appl
26	85	35.3	13	4 US-08-002-054B-17	Sequence 17, Appl
27	85	35.3	13	4 US-08-002-054B-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1	US-09-099-631A-12
Sequence 12, Application US/09099631A	Patent No. 644645
; GENERAL INFORMATION:	
; APPLICANT: Selsted, Michael E.	
; TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs	
; FILE REFERENCE: P-UC 0050	
; CURRENT APPLICATION NUMBER: US/09/099, 631A	
; CURRENT FILING DATE: 1998-06-18	
; NUMBER OF SEQ ID NOS: 13	
; SOFTWARE: PatentIn Ver. 2.1	
; SEQ ID NO 12	
; LENGTH: 63	
; TYPE: PRT	
; ORGANISM: Artificial Sequence	
; FEATURE:	
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic	
US-09-099-631A-12	
; Query Match 55.4%; Score 133.5; DB 4; Length 63;	
; Best Local Similarity 64.7%; Pred. No. 2.9e-10;	
; Matches 22; Conservative 0; Mismatches 5; Indels 7; Gaps 2	
QY	4 KNPWWPKWPKRKKHAEPEAEPERIMILKKWPKWPKR 36
Db	11 KNPWWPKWPKRKKHAEPEAEPERIMILKKWPKWPKR 38
RESULT 2	
; Sequence 38, Application US/08702054B	
; Patent No. 6191254	
; GENERAL INFORMATION:	
; APPLICANT: Falls, Timothy J.	
; APPLICANT: Hancock, Robert E. W.	
; APPLICANT: Gough, Monisha	
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES	
; TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE SAME	
; NUMBER OF SEQUENCES: 44	
; CORRESPONDENCE ADDRESS:	
; ADDRESSE: Fish & Richardson P.C.	
; STREET: 4225 Executive Square, Suite 1400	
; CITY: La Jolla	
; STATE: CA	
; COUNTRY: USA	
; ZIP: 92037	
; COMPUTER READABLE FORM:	
; MEDIUM TYPE: Diskette	

COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEE for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,054B
 FILING DATE: 23-AUG-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/002,687
 FILING DATE: 23-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07420/013001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5095
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-702-054B-38

RESULT 3
 Query Match 41.3%; Score 99.5; DB 4; Length 16;
 Best Local Similarity 43.2%; Pred. No. 1.2e-06;
 Matches 16; Conservative 0; Mismatches 0;
 Indels 21; Gaps 1;

QY 1 ILKKWQWPWRKHEAPEAPEIMILKK 37
 Db 1 ILKKWQWPWRK-----MILKK 16

RESULT 4
 US-08-915-314-56
 ; Sequence 56, Application US/08915314
 ; Patent No. 6180604
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraser, Janet R.
 ; APPLICANT: West, Michael H.P.
 ; APPLICANT: Krieger, Timothy J.
 ; APPLICANT: Taylor, Robert
 ; APPLICANT: Erie, Douglas
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 ; TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
 ; NUMBER OF SEQUENCES: 90
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/915,314
 FILING DATE: 20-AUG-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6180604-Tenburing Ph.D., Carol
 REGISTRATION NUMBER: 39,317
 REFERENCE/DOCKET NUMBER: 660081.405
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 FAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-915-314-56

RESULT 5
 US-08-915-314-55
 ; Sequence 55, Application US/08915314
 ; Patent No. 6180604
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraser, Janet R.
 ; APPLICANT: West, Michael H.P.

RESULT 5
 US-08-915-314-55
 ; Sequence 55, Application US/08915314
 ; Patent No. 6180604
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraser, Janet R.
 ; APPLICANT: West, Michael H.P.

Query Match 37.8%; Score 91; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILKKWPWWPWRK 13
 Db 1 ILKKWPWWPWRK 13

RESULT 9
 US-08-915-314-63
 Sequence 63, Application US/08915314
 Patent No. 6180604
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraser, Janet R.
 ; APPLICANT: West, Michael H.P.
 ; APPLICANT: Krieger, Timothy J.
 ; APPLICANT: Erfile, Douglas
 ; APPLICANT: Taylor, Robert
 ; APPLICANT: Erfle, Douglas
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 ; NUMBER OF SEQUENCES: 90
 ; NUMBER OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLOCIDIN
 ; TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLOCIDIN
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 20-AUG-1997
 ; APPLICATION NUMBER: US/08/915,314
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NO. 6180604 tenburg Ph.D., Carol
 ; REGISTRATION NUMBER: 39,317
 ; REFERENCE/DOCKET NUMBER: 660081.405
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 64:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "D-Form of Isoleucine"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 13
 ; OTHER INFORMATION: /note= "D-Form of Lysine"
 ; US-08-915-314-64

Query Match 37.8%; Score 91; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILKKWPWWPWRK 13
 Db 1 ILKKWPWWPWRK 13

RESULT 10
 US-09-042-071-36
 ; Sequence 36, Application US/09042071
 ; Patent No. 6294372
 ; GENERAL INFORMATION:
 ; APPLICANT: Burian, Jan
 ; APPLICANT: Kay, William W.
 ; TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
 ; TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
 ; TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104

RESULT 9
 US-08-915-314-64
 Sequence 64, Application US/08915314
 Patent No. 6180604
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraser, Janet R.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,071
 FILING DATE: 13-MAR-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mcasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 660081.407
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEX/FAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-042-071-36

Query Match 37.8%; Score 91; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 1 ILKKWPWPKWPK 13
 Db 1 ILKKWPWPKWPK 13

RESULT 11
 US-08-915-314-57
 Sequence 57, Application US/08915314
 Patent No. 6180604
 GENERAL INFORMATION:
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.
 APPLICANT: Krieger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erfle, Douglas
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 NUMBER OF INVENTION: INFECTIOUS USING ANALOGUES OF INDOLICIDIN
 NUMBER OF SEQUENCES: 90
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEDD and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ FOR Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,054B
 FILING DATE: 23-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/002,687
 FILING DATE: 23-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hallie, Lila A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07420/013001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEX/FAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-702-054B-40

Query Match 36.9%; Score 89; DB 4; Length 15;
 Best Local Similarity 43.8%; Pred. No. 2.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

QY 1 ILKKWPWPKWPKHEAPEAEPIMILKKWPW 32
 Db 1 ILKKWPWPKWPK-----WW 14

RESULT 13
 US-08-915-314-46
 Sequence 46, Application US/08915314
 Patent No. 6180604
 GENERAL INFORMATION:
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.

APPLICANT: Krieger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erfile, Douglas
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
 NUMBER OF SEQUENCES: 90
 CORRESPONDENCE ADDRESS:
 ADDRESSE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/915,314
 FILING DATE: 20-AUG-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6180604-tenburg Ph.D., Carol
 REGISTRATION NUMBER: 39,317
 REFERENCE/DOCKET NUMBER: 660081.405
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 US-08-915-314-46
 Query Match 36.3%; Score 87.5; DB 4; Length 21;
 Best Local Similarity 60.0%; Pred. No. 5.2e-05;
 Matches 15; Conservative 1; Mismatches 0;
 Indels 9; Gaps 1;
 OY 4 KWPWNPWRKHEAEPEAPMILKK 28
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 3 RWPWNPWRK-----IMILKK 18
 RESULT 14
 US-08-915-314-52
 Sequence 52, Application US/08915314
 Patent No. 6180604
 GENERAL INFORMATION:
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.
 APPLICANT: Krieger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erfile, Douglas
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
 NUMBER OF SEQUENCES: 90
 CORRESPONDENCE ADDRESS:
 ADDRESSE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/915,314
 FILING DATE: 20-AUG-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6180604-tenburg Ph.D., Carol
 REGISTRATION NUMBER: 39,317
 REFERENCE/DOCKET NUMBER: 660081.405
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 74:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-915-314-74
 Query Match 36.1%; Score 87; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 12; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 OY 2 LKKWNPWRK 13
 Db 1 LKKWNPWRK 12
 RESULT 15
 US-08-915-314-74
 Sequence 74, Application US/08915314
 Patent No. 6180604
 GENERAL INFORMATION:
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.
 APPLICANT: Krieger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erfile, Douglas
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
 NUMBER OF SEQUENCES: 90
 CORRESPONDENCE ADDRESS:
 ADDRESSE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/915,314
 FILING DATE: 20-AUG-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6180604-tenburg Ph.D., Carol
 REGISTRATION NUMBER: 39,317
 REFERENCE/DOCKET NUMBER: 660081.405
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 74:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-915-314-74
 Query Match 35.7%; Score 86; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 Matches 12; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Fri Dec 13 15:05:30 2002

us-09-444-281-35-27-35.ra1

Page 7

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| | | | | | | | | | | |
1 ILKKWPMPWRR 12
Db

Search completed: December 11, 2002, 15:39:59
Job time : 16 secs

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 Run on: December 11, 2002, 15:34:29 ; Search time 35 seconds
 (without alignments)
 140.865 Million cell updates/sec

Title: US-09-444-281-35-27-35
Perfect score: 241
Scoring table: BLOSUM62
Sequence: IILKKWVWWPPWRRKHEAPEAEPPIMLKKWPWWPPWRRK 37
Scoring table: Gapop 10.0 , Gapext 0.5
Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description
1	141.5	58.7	28	21 AAY91800	Amino acid sequence Indolicidin analog
2	137.5	57.1	27	19 AAW63363	Indolicidin analog Poly-(Indol-1-13) Indolicidin fusion
3	133.5	55.4	63	21 AAY44668	Indolicidin fusion
4	133.5	55.4	63	21 AY51142	Indolicidin fusion
5	99.5	41.3	16	18 AAW1899	Antimicrobial cat Indolicidin analog
6	99	41.1	21	19 AAY24582	Amino acid sequence Indolicidin analog
7	99	41.1	21	21 AY91806	Indolicidin analog
8	98	40.7	21	19 AAY24571	Amino acid sequence Indolicidin analog
9	98	40.7	21	21 AAY91808	Indolicidin analog
10	93.5	38.8	20	19 AAY24570	Indolicidin analog

SUMMARIES

SUMMARIES

11	93.5	38.8	20	13	18	AAW12873	Amino acid sequence
12	91	37.8	13	19	19	AAW24609	Antimicrobial cathepsin
13	91	37.8	13	19	19	AAW66378	Indolicidin analog
14	91	37.8	13	19	19	AAW71650	Cationic peptide O
15	91	37.8	13	19	19	AAW94495	Cationic peptide M
16	91	37.8	13	21	21	AAW92795	MBI-11 peptide der
17	91	37.8	13	21	21	AAW92795	Indolicidin analog
18	91	37.8	13	21	21	AAW91773	Amino acid sequence
19	91	37.8	13	21	21	AAW91774	Amino acid sequence
20	91	37.8	13	21	21	AAW91818	Amino acid sequence
21	91	37.8	13	21	21	AAW91819	Amino acid sequence
22	91	37.8	13	21	21	AAW91820	Amino acid sequence
23	91	37.8	13	23	23	ABB1254	CPL1-NH2 antiinfective
24	91	37.8	14	14	14	AAW24583	Indolicidin analog
25	91	37.8	14	21	21	AAW91811	Amino acid sequence
26	89	36.9	15	18	18	AAW13802	Antimicrobial cathepsin
27	87.5	36.3	21	19	19	AAW24552	Indolicidin analog
28	87.5	36.3	21	19	19	AAW66376	Cationic peptide O
29	87.5	36.3	21	21	21	AAW91796	Amino acid sequence
30	87	36.1	12	12	12	AAW24580	Indolicidin analog
31	87	36.1	12	21	21	AAW91804	Amino acid sequence
32	86	35.7	12	18	18	AAW12877	Antimicrobial cathepsin
33	86	35.7	12	19	19	AAW24615	Indolicidin analog
34	86	35.7	12	21	21	AAW91833	Amino acid sequence
35	86	35.7	13	18	18	AAW12896	Antimicrobial cathepsin
36	86	35.7	13	19	19	AAW24613	Indolicidin analog
37	86	35.7	13	19	19	AAW24572	Indolicidin analog
38	86	35.7	13	21	21	AAW91803	Amino acid sequence
39	86	35.7	13	21	21	AAW91812	Indolicidin analog
40	86	35.7	14	19	19	AAW24573	Amino acid sequence
41	86	35.7	14	21	21	AAW91813	Antimicrobial cathepsin
42	85	35.5	16	16	16	AAW12882	Antimicrobial cathepsin
43	85	35.5	16	19	19	AAW24586	Indolicidin analog
44	85	35.3	12	21	21	AAW91828	Amino acid sequence
45	85	35.3	13	18	18	AAW27179	Antimicrobial cathepsin

PT -
 XX
 PS Claim 1; Page 15; 94pp; English.
 XX
 CC This sequence represents a cationic peptide amino acid sequence, which
 CC can be used in the pharmaceutical composition of the invention. The
 CC invention relates to a pharmaceutical composition containing at least one
 CC modified poloxazalylene (APO)-modified cationic peptide. The
 CC modification of peptides with APO increases their activity against tumour
 CC cells, including those with a multidrug resistant phenotype. The
 CC pharmaceutical composition can be used to treat tumours, specifically
 CC lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary,
 CC cervix, uterus, skin, prostate, liver and colon.
 XX
 SQ Sequence 28 AA;
 Query Match 58.7%; Score 141.5; DB 21; Length 28;
 Best Local Similarity 58.8%; Pred. No. 3.6e-11; Indels 11; Gaps 1;
 Matches 20; Conservative 2; Mismatches 1;
 ID AAY44668; AC AAY44668;
 XX
 OY 4 KWPWWPWRKHEAEPEAEPIMILKKWPWWPWRK 37
 DT 18-APR-2000 (first entry)
 DB 3 RWPWWPWRK-----ILMRWPWWPWRK 25
 XX
 RESULT 2
 AAW66363
 ID AAW66363 standard; Peptide; 27 AA.
 XX
 AC AAW66363;
 XX
 -DT 12-JAN-1999 (first entry)
 DE Indolicidin analogue MBI 11B20.
 XX
 KW Indolicidin analogue; resistance; cationic peptide; antibiotic;
 KW bacterial infection; tolerance; antibacterial; microorganism;
 KW bacteria; fungus; parasite; virus.
 OS Synthetic.
 XX
 PN WO9840401-A2.
 XX
 PD 17-SEP-1998.
 XX
 PP 10-MAR-1998; 98WO-CA00190.
 XX
 PR 25-FEB-1998; 98US-0030619.
 PR 10-MAR-1997; 97US-0040649.
 PR 20-AUG-1997; 97US-0915314.
 PR 26-SEP-1997; 97US-0060099.
 XX
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX
 PI Fraser JR, McNicol PJ, West MPH;
 XX
 DR WPI; 1998-520800/44.
 XX
 PT New indolicidin peptide analogues - useful for, e.g. enhancing
 PT activity of antibiotic or overcoming tolerance, acquired resistance
 PT or inherent resistance of microorganisms
 XX
 CC The present sequence represents an indolicidin analogue. The present
 CC invention describes compositions and methods for treating infection,
 CC especially bacterial infections. The compositions and methods use
 CC cationic peptides in combination with an antibiotic agent which are
 CC then administered to a patient to enhance the activity of the antibiotic
 CC agent, to overcome: (a) tolerance; (b) acquired resistance; and (c)
 CC inherent resistance. The combinations of antibiotics and cationic
 CC peptides can provide synergistic activity against a microorganism that

CC is tolerant, inherently resistant, or has acquired resistance to an
 CC antibiotic agent. They can be used for killing e.g. bacteria, fungi,
 CC parasites and viruses.
 XX
 SQ Sequence 27 AA;
 Query Match 57.1%; Score 137.5; DB 19; Length 27;
 Best Local Similarity 61.8%; Pred. No. 1.1e-10; Indels 11; Gaps 2;
 Matches 21; Conservative 2; Mismatches 0;
 ID AAY44668; AC AAY44668;
 XX
 OY 4 KWPWWPWRKHEAEPEAEPIMILKKWPWWPWRK 37
 DB 3 RWPWWPWRK-----MIL-RWPWWPWRK 25
 XX
 RESULT 3
 AAY44668
 ID AAY44668 standard; Protein; 63 AA.
 XX
 AC AAY44668;
 XX
 DT 18-APR-2000 (first entry)
 DE Poly- (Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3 protein.
 XX
 KW Cross linked indolicidin analog; x-indolicidin; poly-Indol 1-13;
 KW stability; bovine neutrophil; antimicrobial; antibacterial; fungicide;
 KW protozoicide; virucide; anti-HIV; human immunodeficiency virus-1;
 KW HIV-1; gram positive bacteria; gram negative; Staphylococcus aureus;
 KW Escherichia coli; Salmonella typhimurium; yeast; fungi; protozoa;
 KW Candida albicans; cryptococcus neoformans; Giardia; Acanthamoeba;
 KW hexapeptide spacer.
 XX
 OS Synthetic.
 OS Bos sp.
 XX
 KEY Location/Qualifiers
 FT Region 1..5
 FT /label= Enterokinase_recognition_site
 FT Cleavage-site 5..6
 FT /label= Enterokinase_cleavage_site
 FT Cleavage-site 6..7
 FT /label= Cyanogen_bromide_cleavage_site
 FT Cleavage-site 20..21
 FT /label= Cyanogen_bromide_cleavage_site
 FT Cleavage-site 25..26
 FT /label= Cyanogen_bromide_cleavage_site
 FT Cleavage-site 39..40
 FT /label= Cyanogen_bromide_cleavage_site
 FT Cleavage-site 44..45
 FT /label= Cyanogen_bromide_cleavage_site
 FT Cleavage-site 58..59
 FT /label= Cyanogen_bromide_cleavage_site
 FT Region 20..25
 FT /label= Hexapeptide_spacer
 FT Region 39..44
 FT /label= Hexapeptide_spacer
 FT Region 58..63
 FT /label= Hexapeptide_spacer
 XX
 PN WO965510-A1.
 XX
 PD 23-DEC-1999.
 XX
 FF 20-MAY-1999; 97US-0099631.
 XX
 PR 18-JUN-1998; 98US-0099631.
 XX
 PA (RESC) UNIV CALIFORNIA.
 XX
 PI Selsted ME, Osapay K;
 XX
 DR WPI; 2000-147133/13.

DR N-PSDB: AA249764.
 XX Crosslinked indolicidin analogs with antimicrobial activity against
 PT bacteria, yeast, fungi, protozoa and viruses -
 XX Example 1C; Fig 1; 53pp; English.

CC The patient discloses crosslinked analogs of indolicidin (Indol 1-13)
 CC which is a naturally occurring peptide isolated from bovine neutrophils
 CC and has antimicrobial activity. The crosslinked indolicidin
 CC (X-indolicidin) analogs are stable and have antimicrobial activity
 CC against gram positive and negative bacteria (e.g. *Staphylococcus aureus*,
 CC *Escherichia coli* and *Salmonella typhimurium*), yeasts and fungi (e.g.
 CC *Candida albicans*, *Cryptococcus neoformans*), protozoa (e.g. *Giardia*
 CC species and *Acanthamoeba* species), and viruses (e.g. HIV-1).
 CC They can be used for reducing or inhibiting the growth or survival of
 CC microorganisms in an environment e.g. a food or food product, a
 CC solution, an inanimate object comprising a surface, or a mammal.
 CC The present sequence is a protein comprising three
 CC copies of Indol 1-13 each separated by a hexapeptide spacer sequence.
 CC A recombinant construct encoding this sequence was used for the
 CC expression of Indol-homoserine (Hse) analog. The ability of
 CC Indol-Hse analog to maintain antimicrobial activity provides a means to
 CC produce X-indolicidin analog precursors in sufficient quantities.
 XX Sequence 63 AA:

Query Match 55.4%; Score 133.5; DB 21; Length 63;
 Best Local Similarity 64.7%; Pred. No. 9e-10; 0; Mismatches 5; Indels 7; Gaps 2;
 Matches 22; Conservative AC; CC

Qy 4 KWPWWPWRKHEAPEAPIMLK-KWPWWPWR 36
 Db 11 KWPWWPWRM-----ARIAMILPWKWPWWPWR 38

RESULT 4
 ID AAY57142
 XX AAY57142 standard; Protein; 63 AA.
 AC AAY57142;
 DT 28-FEB-2000 (first entry)
 DE Indolicidin fusion peptide amino acid sequence.
 XX Indolicidin analogue; antimicrobial activity; helminth; bacteria; virus;
 KW treatment; inhibit growth; micro-organism; contact lens solution;
 KW transgenic plant; surgical instrument; yeast; fungi; protozoa.
 OS Synthetic.
 PN W09958141-A1.
 XX 18-NOV-1999.
 PD XX 05-MAY-1999; 99WO-US09942.
 PR XX 12-MAY-1998; 98US-0076227.
 PA XX (REGC) UNTV CALIFORNIA.
 XX Selsted ME;
 DR XX WPI; 2000-053028/04.
 DR N-PSDB; AA249764.
 XX New indolicidin analogues, active against bacteria, yeast, fungi,
 PT protozoa and virus, used for, e.g. treating infections -
 XX Disclosure; Fig 6; 62pp; English.
 PS XX This is the amino acid sequence of an example of a fusion protein which

CC consists of an indolicidin analogue linked to another peptide.
 Peptides AA127105-Y57138 and AA127141-Y57144 are new indolicidin
 analogues, which have a homoserine residue and/or a truncated amino
 terminal region. The analogues have the following amino acid sequence:
 CC Xaa1-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6-Pro-Xaa6-Xaa6-Pro-Xaa7-Xaa7-Xaa8
 CC Where:
 CC Xaa1 = Ile, leu, Val, Ala, Gly or absent;
 CC Xaa2 = Ile, leu, Val, Ala, Gly or absent;
 CC Xaa3 = Pro or absent;
 CC Xaa4 = Trp, Phe or absent;
 CC Xaa5 = Arg, Lys or absent;
 CC Xaa6 = Trp or Phe;
 CC Xaa7 = Arg, Lys or absent;
 CC Xaa8 = homoserine (Hse), Met, Met-Xaa9-Met or absent, and
 CC Xaa9 = at least one amino acid;
 CC provided that if Xaa1 is present, Xaa8 = Hse, Met or Met-Xaa9-Met;
 CC and further provided that: if Xaa2 is absent, Xaa1 is absent; if Xaa3 is
 CC absent, Xaa1 and Xaa2 are absent; if Xaa4 is absent, Xaa1, Xaa2 and Xaa3
 CC are absent; and if Xaa5 is absent, Xaa1, Xaa2, Xaa3 and Xaa4 are absent.
 CC The indolicidin analogues can be used to create a fusion polypeptide
 CC consisting of the analogue linked to a peptide. The indolicidin
 CC analogues have antimicrobial activity against gram positive bacteria,
 CC gram negative bacteria, yeast, fungi, protozoa and viruses (e.g. HIV-1).
 CC They are also active against helminths. The analogues can be used for
 CC reducing or inhibiting growth or survival of a microorganism. They can be
 CC used for treating infections. They can also be included in a liquid such
 CC as water or an aqueous solution, e.g. contact lens solution. The
 CC analogues have potential uses in food products, and in objects such as
 CC the surface of an instrument used to prepare food or to perform surgery.
 CC Transgenic plants or animals useful in the food industry can be produced
 CC by introducing a nucleic acid molecule encoding an indolicidin analogue
 CC into the germline cells of such organisms.
 XX Sequence 63 AA;

Query Match 55.4%; Score 133.5; DB 21; Length 63;
 Best Local Similarity 64.7%; Pred. No. 9e-10; 0; Mismatches 5; Indels 7; Gaps 2;
 Matches 22; Conservative AC; CC

Qy 4 KWPWWPWRKHEAPEAPIMLK-KWPWWPWR 36
 Db 11 KWPWWPWRM-----ARIAMILPWKWPWWPWR 38

RESULT 5
 ID AAW12899
 XX AAW12899 standard; peptide; 16 AA.
 AC AAW12899;
 XX 10-DEC-1997 (first entry)
 DE Antimicrobial cationic peptide CP-26.
 XX Bacterial; viral; antitumour; food; preservative; inhibitor; growth;
 KW bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal;
 KW antiviral; *Candida albicans*; sterilant; *Salmonella*; *Yersina*;
 KW *Shigella*.
 OS Synthetic.
 XX WO9708199-A2.
 PN 06-MAR-1997.
 XX 23-AUG-1996; 96WO-IB000996.
 PR XX (UVER-) UNIV BRITISH COLUMBIA.
 PA XX Failla TJ, Gough M, Hancock REW.
 PI XX

DR WPI: 1997-179179/16.
 XX
 PT Cationic peptide(s) having anti-microbial activity - used for the
 PT inhibition of bacterial and viral growth, as an antitumour agent,
 PT and as a food preservative
 XX

PS Claim 3; Page 66; 89pp; English.

XX
 CC The present sequence represents a specifically claimed novel isolated
 CC cationic peptide which has antimicrobial activity. The amino acid
 CC sequence of antimicrobial cationic peptides (including the present
 CC sequence) is selected from: X1X1ProX3X2Pro(X2X2Pro)X1(X5)O;
 CC X1X1ProX2X3X1(X5)1ProX2X3X3; X1X1X3(Pro)Pux3X2X5X2X2X5X1(X5)O;
 CC X1X1X3X2Pro(X2X2Pro)X2(X5)m; where m = 1-5; n = 1-2; o = 2-5; r
 CC = 0-8; u = 0-1; X1 = Ile, Val, Phe, Tyr, Trp or Met; X2 = Trp or
 CC Phe; X3 = Arg or Lys; X4 = Trp or Lys; and X5 = Phe, Trp, Arg, Lys or
 CC Pro. The peptides are preferably amidated or carboxymethylated. The
 CC peptides may be used in methods for inhibiting the growth of a bacterium
 CC or yeast, or for inhibiting an endotoxaemia or sepsis associated
 CC disorder in a subject. The peptides have a broad activity against
 CC antibiotic resistant bacteria, combined with activity against the
 CC medically important fungus *Candida albicans*. In addition, the peptides
 CC are useful as antitumour agents and/or antiviral agents. The peptides
 CC may be used as sterilants or preservatives of materials susceptible to
 CC microbial or viral contamination, e.g. in processed foods to inhibit
 CC *Salmonella*, *Yersina* and *Shigella*. The peptides are compact and tend to
 CC have a unique polyproline type II extended helix structure that permits
 CC them to span the membrane with relatively few amino acids. The peptides
 CC possess the ability to work synergistically with antibiotics, and in
 CC addition, some of them possess anti-endotoxin activity.
 XX

.SQ Sequence 16 AA;

Query Match 41.3%; Score 99.5; DB 18; Length 16;
 Best Local Similarity 43.2%; Pred. No. 3.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 21; Gaps 1;
 QY 1 ILKKWPWWPWRKHEAPEPAPIMILKKHWWPWRK 37
 Db 1 ILKKWPW-----WPPWWPWRK 16

RESULT 6
 AAY24582
 ID AAY24582 standard; Peptide; 21 AA.

XX
 AC AAY24582;
 XX
 DT 18-AUG-1999 (first entry)

XX
 DE Indolicidin analogue #34.

XX
 KW Indolicidin; bacterial infection; photo-oxidised solubiliser;
 KW antimicrobial; antibiotic; antiarhythmcc; surface disinfectant;
 KW additive; shampoo; soap; insecticide; herbicide; preservative;
 KW food; technical material.

XX
 OS Synthetic.

XX
 PN WO9807745.A2.

XX
 PD 26-FEB-1998.

XX
 PF 21-AUG-1997; 97WO-US14779.

XX
 PR 13-JAN-1997; 97US-0034949.

XX
 PR 21-AUG-1996; 96US-0024754.

XX
 PA (MICR-) MICROLOGIX BIOTECH INC.

XX
 PI Erfle D, Fraser JR, Krieger TJ, Taylor R, West MH;

XX
 DR WPI: 1998-169090/15.

XX
 PT New indolicidin analogues with antimicrobial activity and related
 PT nucleic acid - vectors, transformed cells and antibodies, also
 PT conjugates with polyoxalkylene glycol and fatty acid to reduce
 PT toxicity, useful therapeutically, as disinfectants etc.

XX
 PS Claim 13; Page 89; 129pp; English.

XX
 CC AAY24549 to AAY24615 represent indolicidin analogues of formulae
 CC (I) - (VII) containing up to 25 amino acids (aa); RAXXXXB (I), BXZXXZB
 CC (II), BBBZXXBB (III), BXZXXXB(Bn(A)n)MLBBAGS (IV), BXZXXXB(Bn(A)n)M
 CC (V), LBZBZNNZBXRK (VI), LKNZKZKZRRK (VII) and BXZXXXB(B)BB (VIII).
 CC Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa,
 CC preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V;
 CC in (VII) at least 2 X = F or Y. The analogues are used to treat
 CC infections caused by bacteria (Gram positive or negative or anaerobic);
 CC fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or
 CC trematodes) or viruses. Typical of very many pathogens that can be
 CC controlled are *Leishmania*, *Trypanosoma*, *Ascaris lumbricoides*, *Fasciola*
 CC, *hepatica*, *Klebsiella pneumoniae*, *Bordetella pertussis*, *Staphylococcus*
 CC *aureus*, *Listeria*, *Clostridium*, *rotavirus* and *papilloma virus*. Compounds
 CC derived from the analogues may be used similarly; the compounds may
 CC also be prepared from antibiotics or antiarrhythmic agents. The analogues
 CC may be used therapeutically or to coat medical devices; also they are
 CC useful as surface disinfectants, as additives to shampoo or soaps, as
 CC insecticides or herbicides, or as preservatives for foods and technical
 CC materials. The analogues are administered by injection, lavage, orally
 CC or topically, generally at 0.1-50 mg/kg. These analogues have a broader
 CC spectrum of activity than indolicidin and modification as compounds
 CC reduces their toxicity.

XX
 SQ Sequence 21 AA;

Query Match 41.1%; Score 99; DB 19; Length 21;
 Best Local Similarity 64.3%; Pred. No. 5.9e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 QY 1 ILKKWPWWPWRKHEAPEPAPIMILKK 28
 Db 1 ILKKWPWWPWRK-----MILKK 18

RESULT 7
 AAY91806
 ID AAY91806 standard; Peptide; 21 AA.

XX
 AC AAY91806;
 XX
 DT 06-JUN-2000 (first entry)

XX
 DE Amino acid sequence of cationic peptide MBI 11D4CN.

XX
 KW Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;
 KW leukaemia; polyoxalkylene-modified; ARO; lymphoma; multiple myeloma;
 KW breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
 KW multidrug resistance.

XX
 OS Synthetic.

XX
 PN WO9955506-A2.

XX
 PD 23-DEC-1999.

XX
 PF 14-JUN-1999; 99WO-CA00552.

XX
 PR 12-JUN-1998; 98US-0096541.

XX
 PA (MICR-) MICROLOGIX BIOTECH INC.

XX
 PI Friedland HD, Krieger TJ, Taylor R, Erfle D, Fraser JR, West MHP;

XX
 DR WPI: 2000-223549/19.

PT Novel pharmaceutical composition containing optionally activated polyoxalkylene-modified cationic peptides, useful for treating tumours
 PT Disclosure; Page 15; 94pp; English.

CC This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.

CC cervix, uterus, skin, prostate, liver and colon.

CC Sequence 21 AA:

Query Match 41.1%; Score 99; DB 21; Length 21;
 Best Local Similarity 64.3%; Pred. No. 5.9e-06; Mismatches 0; Indels 10; Gaps 1;
 Matches 18; Conservative 0; OS Synthetic.

QY 1 ILKKWPWPWRRKHEAPEPIMILRK 28
 Db 1 ILKKWPWPWPWRRK-----MILRK 18

RESULT 8

AY24571 AY24571 standard; peptide: 21 AA.

XX AY24571;
 AC AY24571;

DT 18-AUG-1999 (first entry)

XX Indolicidin analogue #23.

DE Indolicidin; bacterial infection; photo-oxidized solubiliser; antimiocrobial; antibiotic; antiarrhythmic; surface disinfectant; additive; shampoo; soap; insecticide; herbicide; preservative; food; technical material.

XX Synthetic.

XX WO9807745-A2.

XX 26-FEB-1998.

XX PF . 21-AUG-1997; 97WO-US14779.

XX PR 13-JAN-1997; 97US-0034949.

XX PR 21-AUG-1996; 96US-0024754.

XX PA (MICR-) MICROLOGIX BIOTECH INC.

XX PT Erfle D, Fraser JR, Krieger TJ, Taylor R, West MH;
 XX DR WPI; 1998-169090/15.

XX New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.

PS Claim 12; Page 89; 129pp; English.

XX AAY24549 to AAY24615 represent indolicidin analogues of formulae (I)-(VII) containing up to 25 amino acids (aa): RX2XX2XB (I), BX2XX2XB (II), BBBX2XX2XB (III), BX2XX2XB(BA)nM (IV), LBNX2XX2XB (V), LKNX2XX2XB (VI), and BBX2XX2XB (VII). Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa, preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V; in (VII) at least 2 X = F or V. The analogues are used to treat

CC infections caused by bacteria (Gram positive or negative, or anaerobic); fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or trematodes) or viruses. Typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica, Klebsiella pneumoniae, Bordetella pertussis, *Staphylococcus aureus*, *Listeria*, *Clostridium*, *rotavirus* and *Escherichia coli*. Compounds derived from the analogues may be used similarly; the compounds may also be prepared from antibiotics or antiarrhythmic agents. The analogues may be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds reduces their toxicity.

CC Sequence 21 AA:

Query Match 40.7%; Score 98; DB 19; Length 21;
 Best Local Similarity 64.3%; Pred. No. 7.8e-06; Mismatches 0; Indels 10; Gaps 1;
 Matches 18; Conservative 0; OS Synthetic.

QY 1 ILKKWPWPWRRKHEAPEPIMILRK 28
 Db 1 ILKKWPWPWPWRRK-----IMILRK 18

RESULT 9

AY91808 AY91808 standard; Peptide: 21 AA.

XX AY91808;
 AC AY91808;

DT 06-JUN-2000 (first entry)

XX Amino acid sequence of cationic peptide MBI 11D6CN.

DE Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.

XX OS Synthetic.

XX WO965506-A2.

XX PD 23-DEC-1999.

XX PF 14-JUN-1999; 99WO-CA000552.

XX PR 12-JUN-1998; 98US-0096541.

XX PA (MICR-) MICROLOGIX BIOTECH INC.

XX PT Friedland HD, Krieger TJ, Taylor R, Erfle D, Fraser JR, West MH;
 XX DR WPI; 2000-223549/19.

XX Novel pharmaceutical composition containing optionally activated polyoxalkylene-modified cationic peptides, useful for treating tumours

PT Disclosure; Page 15; 94pp; English.

XX This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically cervix, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.

SQ	Sequence	21 AA:	Score	DB	Length	21;	Score	DB	Length	20;
Query Match	40.7%	Score 98;	DB 21;	Length 21;			38.8%	Score 93.5;	DB 19;	Length 20;
Best Local Similarity	64.3%	Pred. No.	7.8e-06;	Pred. No.	2.7e-05;		60.7%	Pred. No.	2.7e-05;	
Matches	18;	Conservative	0;	Mismatches	0;	Indels	10;	Gaps	1;	Indels
Qy	1	ILKKWPWPWPKHAEPEAEPIMILKK 28					1	ILKKWPWPWPKHAEPEAEPIMILKK 28		
Db	1	ILKKWPWPWPKR-----MLKK 18					1	ILKKWPWPWPKR-----MLKK 18		
RESULT 10							RESULT 11			
RAV124570							RAV91807			
ID	AY24570	standard; peptide; 20 AA.					ID	AY91807	standard; Peptide; 20 AA.	
XX							XX			
AC	AY24570;						AC	AY91807;		
XX							XX			
DT	18-AUG-1999	(first entry)					DT	06-JUN-2000	(first entry)	
XX							XX			
DE	Indolicidin analogue #22.						DE	Amino acid sequence of cationic peptide MRI 11D5CN.		
XX							XX			
KW	Indolicidin; bacterial infection; photo-oxidised solubiliser;						KW	Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;		
KW	antimicrobial; antibiotic; antiarrhythmic; surface disinfectant;						KW	leukaemia; polyoxalkylene modified; APO; lymphoma; multiple myeloma;		
KW	additive; shampoo; soap; insecticide; herbicide; preservative;						KW	breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;		
KW	food; technical material.						KW	multidrug resistance.		
OS	Synthetic.						OS	Synthetic.		
XX							XX			
PR	W09807745-A2.						PR	W0965506-A2.		
XX							XX			
PD	26-FEB-1998.						PD	23-DEC-1999.		
XX							XX			
PF	21-AUG-1997;	97WO-US14779.					PF	14-JUN-1999;	99WO-CA00552.	
XX							XX			
PR	13-JAN-1997;	97US-0034949.					PR	12-JUN-1998;	98US-0096541.	
PR	21-AUG-1996;	96US-0024754.					PR			
XX							PA	(MICR-) MICROLOGIX BIOTECH INC.		
PA	(MICR-) MICROLOGIX BIOTECH INC.						XX			
XX							PA	(MICR-) MICROLOGIX BIOTECH INC.		
PI	Erfle D, Fraser JR, Krieger TJ, Taylor R, West MHP;						XX			
XX							PI	Friedland HD, Krieger TJ, Taylor R, Erfle D, Fraser JR, West MHP;		
DR	WPI; 1998-169090/15.						XX			
XX							DR	WPI; 2000-223549/19.		
PS	New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.						XX			
XX	claim 12; Page 89; 129pp; English.						PT	Novel pharmaceutical composition containing optionally activated polyoxalkylene-modified cationic peptides, useful for treating tumours		
PT	AAV24549 to AAV24615 represent indolicidin analogues of formulae (I)-(VIII) containing up to 25 amino acids (aa): RXZXXZB (I), BXZXXZXB (II), BBBZXXZXB (III), BXZXXZBBN(AA)nM (IV), BXZXXZBB(AA)nM (V), LBNZXXZXXZRK (VI), LKNZXXZXXRK (VII) and BBZXXZXXBB (VIII), where Z = P or V; AA = hydrophobic residue, preferably W; B = basic aa, preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V; in (VIII) at least 2 X = F or Y. The analogues are used to treat infections caused by bacteria (Gram positive or negative, or anaerobic); fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or trematodes) or viruses; typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus aureus, listeria, Clostridium, rotavirus and papilloma virus. Compounds derived from the analogues may be used similarly; the compounds may also be prepared from antibiotics or antiarrhythmic agents. The analogues may be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds						PT	Novel pharmaceutical composition containing optionally activated polyoxalkylene-modified cationic peptides, useful for treating tumours		
XX							PT			
PS	Disclosure: Page 15; 94pp; English.						XX			
XX							PS			
CC	This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.						CC			
CC	Sequence 20 AA:						CC			
CC	Query Match	38.8%	Score	93.5;	DB	21;	Length	20;		
CC	Best Local Similarity	60.7%	Pred. No.	2.7e-05;			Mismatches	0;		
CC	Matches	17;	Conservative	0;	Mismatches	0;	Indels	11;	Gaps	1;
Qy	1	ILKKWPWPWPKHAEPEAEPIMILKK 28					Qy	1	ILKKWPWPWPKHAEPEAEPIMILKK 28	
Db	1	ILKKWPWPWPKR-----MLKK 17					Db	1	ILKKWPWPWPKR-----MLKK 17	
RESULT 12							RESULT 12			
ID	RAV12873	standard; peptide; 13 AA.					ID	RAV12873	standard; peptide; 13 AA.	

XX
XX AAW12873;
AC
XX 10-DEC-1997 (first entry)
DT
XX DE Antimicrobial cationic peptide CP-11.
XX
KW Bacterial; viral; antitumour; food; preservative; inhibitor; growth;
KW bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal;
KW antiviral; Candida albicans; sterilant; Salmonella; Yersina;
KW Shigella.
XX
OS Synthetic.
XX
PN WO9708199-A2.
XX
PD 06-MAR-1997.
XX
PF 23-AUG-1996; 96WO-IB00996.
PR 23-AUG-1995; 95US-0002687.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Falla TJ, Gough M, Hancock REW;
XX DR WPI; 1997-179179/16.
XX
Cationic peptide(s) having anti-microbial activity - used for the
PT inhibition of bacterial and viral growth, as an antitumour agent,
PT and as a food preservative
PT
XX
PS Claim 2; Page 65; 89pp; English.
XX
The present sequence represents a specifically claimed novel isolated
CC cationic peptide which has antimicrobial cationic peptides (including the present
CC sequence) is selected from: X1X1PROXK3X2Pro(XX2Pro)nX23(X5)0;
CC X1X1PROX2X3X4(X5)0rProX2X3X2; X1X1X3(XPro)px3X2X5X2X2X5X2(X5)0;
CC X1X1X3X2Pro(XX2Pro)nX2X5X2(X5)m; where m = 1-5; n = 1-2; o = 2-5; r
= 0-8; u = 0-1; x1 = Ile, Leu, Val, Phe, Tyr, Trp or Met; x2 = Trp or
Phe; x3 = Arg or Lys; x4 = Trp or Lys; and x5 = Phe, Trp, Arg, Lys or
Pro. The peptides are preferably amidated or carboxymethylated. The
peptides may be used in methods for inhibiting the growth of a bacterium
or yeast, or for inhibiting an endotoxaemia or sepsis associated
disorder in a subject. The peptides have a broad activity against
antibiotic resistant bacteria, combined with activity against the
medically important fungus Candida albicans. In addition, the peptides
are useful as antitumour agents and/or antiviral agents. The peptides
may be used as sterilants or preservatives of materials susceptible to
microbial or viral contamination, e.g. in processed foods to inhibit
Salmonella, Yersina and Shigella. The peptides are compact and tend to
have a unique polyproline type II extended helix structure that permits
them to span the membrane with relatively few amino acids. The peptides
possess the ability to work synergistically with antibiotics, and in
addition, some of them possess anti-endotoxin activity.
N.B. The present sequence represents SEQ ID NO:1 in the claims and
examples of the specification, but differs slightly from the SEQ ID NO:1
CC in the sequence listing on Page 51 of the specification (see AAW27179).
XX
SQ Sequence 13 AA;
Query Match 37.8%; Score 91; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILKKWPWWPWRK 13
Db 1 ILKKWPWWPWRK 13

XX
XX AAY24609 standard; peptide; 13 AA.
ID AAY24609;
XX AC AAY24609;
XX DT 18-AUG-1999 (first entry)
XX DE Indolicidin analogue #61.
XX
KW Indolicidin; bacterial infection; photo-oxidised solubiliser;
KW antimicrobial; antibiotic; antiarrhythmic; surface disinfectant;
KW additive; shampoo; soap; insecticide; herbicide; preservative;
KW food; technical material.
XX
OS Synthetic.
XX
PN WO9607745-A2.
XX
PD 26-FEB-1998.
XX
PF 21-AUG-1997; 97WO-US14779.
XX
PR 13-JAN-1997; 97US-0034949.
PR 21-AUG-1996; 96US-0024754.
XX
PA (MICR-) MICROLOGIX BIOTECH INC.
XX
PI Erfie D, Fraser JR, Krieger TJ, Taylor R, West MH;
XX DR WPI; 1998-169090/15.
XX
New indolicidin analogues with antimicrobial activity and related
PT nucleic acid - vectors, transformed cells and antibodies, also
PT conjugates with polyoxalkylene glycol and fatty acid to reduce
PT toxicity, useful therapeutically, as disinfectants etc.
XX
PS Example 1; Page 32; 129pp; English.
XX
AAY24549 to AAY24515 represent indolicidin analogues of formulae
CC (I)-(VIII) containing up to 25 amino acids (aa): RXZZXZB (I), BXZZXZB
(II), BBBZXXZB (III), BXZZXZBBN(A)nMILBAGS (IV), BXZZXZBB(A)nM
(V), LBKZXZBZNNRK (VI), LKXZXZBZRRK (VII) and BXZZXZBB
(VIII).
CC Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa,
CC preferably R or K; AA = any aa, n = 0 or 1; in (II), at least 1 Z = V;
CC in (VIII) at least 2 X = F or Y. The analogues are used to treat
CC infections caused by bacteria (Gram positive or negative, or anaerobic);
CC fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or
CC trematodes) or viruses. Typical of very many pathogens that can be
CC controlled are Leishmania, trypanosomes, Ascaris lumbricoides, Fasciola
hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus
aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds
CC derived from the analogues may be used similarly; the compounds may
CC also be prepared from antibiotics or antiarrhythmic agents. The analogues
CC may be used therapeutically or to coat medical devices; also they are
CC useful as surface disinfectants, as additives to shampoo or soaps, as
CC insecticides or herbicides, or as preservatives for foods and technical
CC materials. The analogues are administered by injection, lavage, orally
CC or topically, generally at 0.1-50 mg/kg. These analogues have a broader
CC spectrum of activity than indolicidin and modification as compounds
CC reduces their toxicity.

XX
SQ Sequence 13 AA;
Query Match 37.8%; Score 91; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILKKWPWWPWRK 13
Db 1 ILKKWPWWPWRK 13

ID AAW6378 standard; Peptide; 13 AA.
 XX
 AC
 XX
 DT
 XX
 DE Cationic Peptide of claim 15 #5.
 XX
 KW Indolicidin analogue; resistance; cationic peptide; antibiotic;
 bacterial infection; tolerance; antibacterial; microorganism;
 KW bacteria; fungi; parasite; virus.
 XX
 OS Synthetic.
 XX
 PN WO9840401-A2.
 XX
 PR 17-SEP-1998.
 XX
 PR 10-MAR-1998; 98WO-CA00190.
 XX
 PR 25-FEB-1998; 98US-0030619.
 XX
 PR 10-MAR-1997; 97US-0040649.
 XX
 PR 20-AUG-1997; 97US-0915314.
 XX
 PR 26-SEP-1997; 97US-0060099.
 XX
 PA (MICR-) MICROLOGIX BIOTECH INC.
 XX
 PI Fraser JR, McNicol PJ, West MHP;
 XX
 DR WPI; 1998-531571/45.
 XX
 PR Increasing plasmid copy number in a cell with the repA gene product;
 PT and an small cryptic plasmid ori sequence, useful for high level
 expression of e.g. cytokines, antigens or therapeutic proteins
 XX
 PS Example 13; Page 54; 82PP; English.
 XX
 CC MBII.1 is a small (mol wt. 1879) cationic peptide. DNA encoding
 CC MBII.1 has been incorporated into vector PR2h-B1, in which the
 CC replication Leader (R21) sequence of repA (see also AAW71686) is
 CC joined to 2 Hpa peptides (see also AAW71692), to provide a
 CC vector for expression of MBII.1 in host cells. The invention
 CC provides controlled replication plasmid vectors (RAMP vectors)
 CC comprising a replication origin of a small cryptic plasmid and a
 CC gene encoding repA. The vectors can reach very high levels of
 CC plasmid replication, but are not lethal to the host cell, and can
 CC be used to direct the high level expression of e.g. cytokines,
 CC antigens and therapeutic proteins.
 XX
 PS
 SQ sequence 13 AA;
 XX
 Query Match 37.8%; Score 91; DB 19; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 1 ILKKWPWWPWRK 13
 Db 1 ILKKWPWWPWRK 13
 Search completed: December 11, 2002, 15:38:44
 Job time : 35 secs

RESULT 15
 AAW71690
 ID AAW71690 standard; Peptide; 13 AA.
 XX
 AC
 XX
 DT
 XX
 DE Cationic peptide MBII (NW 1879).
 XX
 KW MBII; cationic peptide; plasmid pKII; small cryptic plasmid;
 KW replication; repA; vector; RAMP.
 XX

Query Match 37.8%; Score 91; DB 19; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 1 ILKKWPWWPWRK 13
 Db 1 ILKKWPWWPWRK 13